

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 4, 2004, 15:37:11 ; Search time 0.001 Seconds  
(without alignments)  
679.944 Million cell updates/sec

Title: us-09-674-593-10

Perfect score: 246  
Sequence: 1 gtcattaaccttgcgaagga.....ttcatatcaaccacacta 246

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 0.5

Searched: 1 segs, 1382 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1 summaries

Database : us-09-674-593-1:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	244.4	99.3	1382	1	us-09-674-593-1

# ALIGNMENTS

RESULT 1  
us-09-674-593-1

Query Match 99.3%; Score 244.4; DB 1; Length 1382;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 245; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	GTGATTAACTTGGCAAGATACCTTTTATTTCTTTAAGATTCCTGTGTTTATATACAC	60
DB	268	GTGACTAACCTTGCAAGATACCTTTTATTTCTTTAAGATTCCTGTGTTTATATACAC	327
QY	61	AGATTTTAAGTTACTCTACTACTGACCAAGTAATTCCTCTCCAGTCACAGTGTG	120
DB	328	AGATTTTAAGTTACTCTACTACTGACCAAGTAATTCCTCTCCAGTCACAGTGTG	387
QY	121	AACTCTACCCCGCAACGAGAGATTTTGGAGGAGATCAATGACACCGAGAGTCA	180
DB	388	AACTCTACCCCGCAACGAGAGATTTTGGAGGAGATCAATGACACCGAGAGTCA	447
QY	181	CAGCCCGTCAACGAGAGATTTGAGGAGATTCGATTTCTTCATATCAACCC	240
DB	448	CAGCCCGTCAACGAGATTTGAGGAGATTCGATTTCTTCATATCAACCC	507
QY	241	ACACTA 246	
DB	508	ACACTA 513	

Search completed: June 4, 2004, 15:37:11  
UOD time : 0.001 secs